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Fig. 1

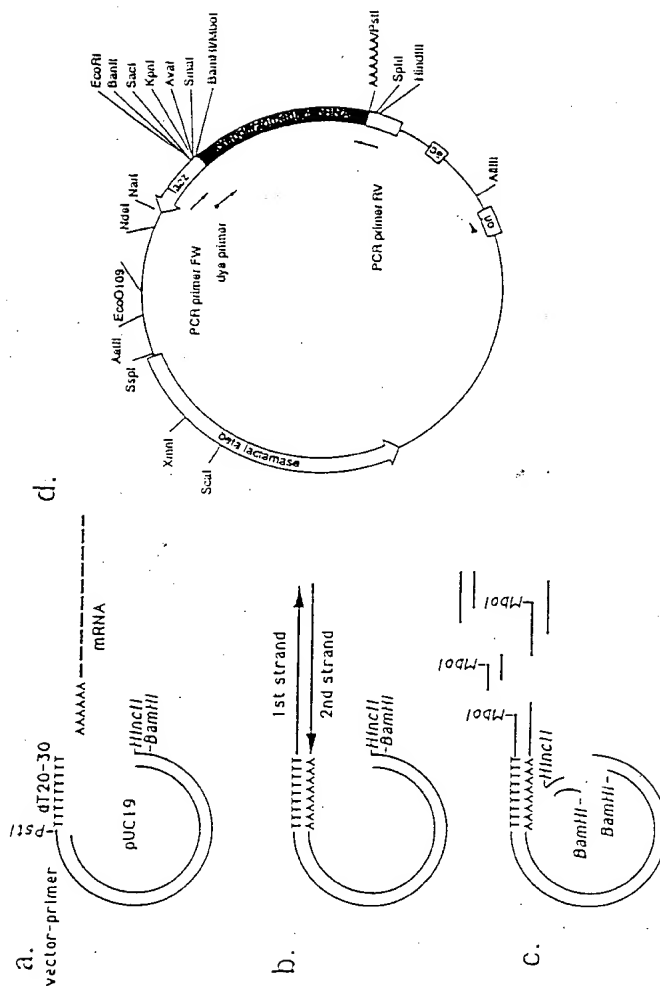
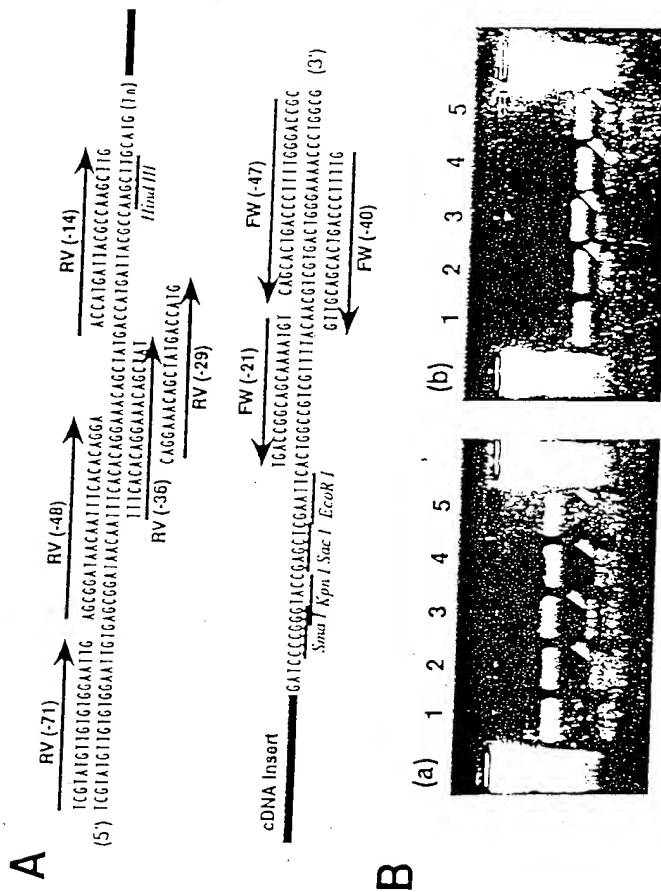


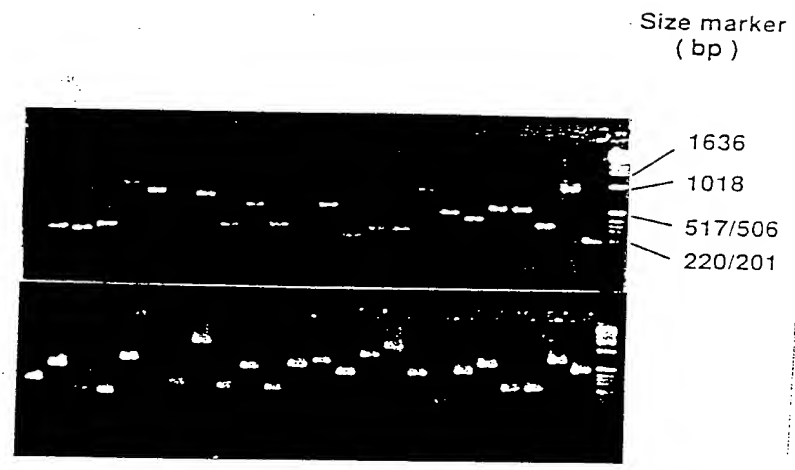
Fig. 2



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Fig. 3



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Fig. 4

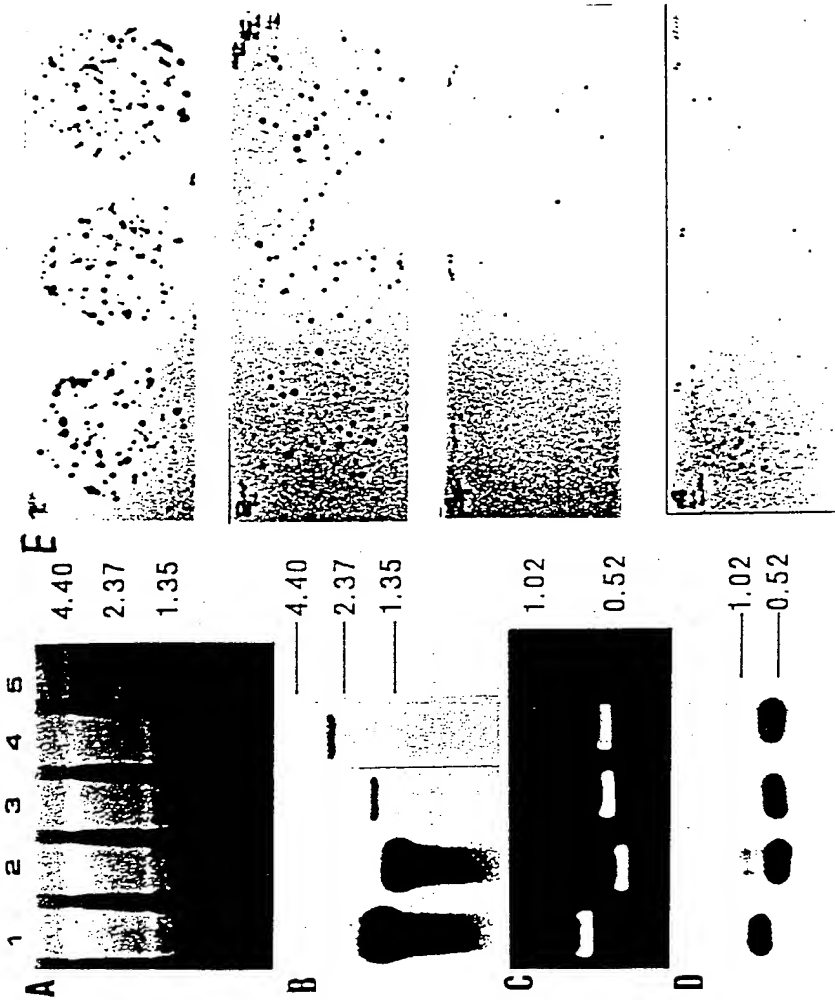


Fig. 4

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probe No.	1	2	3	4
gene	Elongation factor 1- α	α 1-antitrypsin	HnRNP core protein A1	Inter- α -trypsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b) Band intensity of control blot(cpm)	133	177	100	127
(c) Normalized signal(a)/(b) $\times 10$	52	24	1	1.2
(d) Positive signals on colony blot	307	119	7	9
(e) Relative representation	44	17	1	1.3

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Fig. 5

Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library				
Group	Clone	Gene	A in 982 (%)	B "in 8,000 (%)" C "in 26,400 (%)"
I	a15	Elongation factor - 1A α	22 (2.2)	307 (3.5)
	c321	Translationally restricted tumor protein	12 (1.2)	89 (1.0)
	lb038	α -1-antitrypsin	8 (0.8)	119 (1.4)
	hm01b02	Light chain of ferritin	6 (0.6)	62 (0.7)
	c13a04	NADP(H) Menadione oxidoreductase	4 (0.4)	27 (0.3)
	hm02d02	Ribosomal protein S11	3 (0.3)	29 (0.3)
	lb042	Human RNP core protein A1	2 (0.2)	7 (0.1)
	s155	unknown	1	5 (0.02)
	s159	unknown	1	4 (0.02)
	s639	unknown	1	3 (0.01)
II	s635	unknown	1	2 (0.01)
	s170	unknown	1	1 (0.004)
	s154	unknown	1	1 (0.004)
	s167	unknown	1	1 (0.004)
	s645	unknown	1	1 (0.004)
	s647	unknown	1	1 (0.004)
	s632	unknown	1	0 (<0.004)
			1	0 (<0.004)
			1	0
			1	0

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Fig. 6

GS	CII	Chromosomal position	Sequences of primers		AT	TIO	HIE	TIO	CO	G	T
			Sense	Anti-sense							
9:00070a	pin2366	1	CAGAGCCCGATACACTAT	AAGTTTATGTGGGTCAG	48	114	115	104	110	1	2
9:001026	pin2444	1	AATGGACAGTTACACTTGA	CCAGCTCTCTGACTGTGAGA	48	83	81	>200	>200	1	1
9:001075	pin0883	1	TGGACTGTGGATACCTATCT	ACAGTACCCTGATGTTGGCT	48	124	124	103	107	4	4
9:001087	pin1772	1	GTACTCTACGCCATAGCAC	ACCATCTTCAGCCCACTT	50	104	104	180	>200	6	6
9:001094	pin0347	1	GCCCTAACACAGGAACTC	TAATTTCCCACTCCGTAAC	51	114	116	>200	200	1	1
9:001116	pin1771	1	GGGTTTCAATAGGGTAGACC	GCCCAATCTGTCAAACTG	49	95	95	78	107	1	1
9:001191	pin0600	1	TTGTGGATGTGAATTTTG	GGCTGACATTCACCTTGG	47	97	97	-	200	1	1
9:001200	pin1351	1	TTAAGAGACCTTATGAGACC	AATATCTTGGTAGTCACTTAC	47	97	98	-	-	1	1
9:001346	pin0982	1	TCAGTCTGCTTGGAGATG	AATCACAGCACGATTTTG	53	120	122	>200	>200	1	1
9:001464	pin1518	1	AAGGTGTACAGGATTTTGCAGA	TGCATAGCCCACTCTCAT	47	130	125	>200	>200	1	1
9:001468	pin1439	1	CCAAAGACCTCCGTTGACCA	TTGGGAGACCCATAGACAG	51	100	100	>200	-	1	1
9:001521	pin0427	1	TACTCAGTGGAAAGATAAAC	CAGTGGACACATTTCTTA	40	98	98	-	-	2	2
9:001554	pin2785	1	CCCAATCAATTTGTTAAATG	TTTGATCAGAGACGTGAAGTT	43	102,175	100	>200	>200	1	1
9:001572	pin2291	1	CCAGAGATTTCAAGGGATG	GGTCAAGTGCCTCAATGACT	46	57	57	78	155	1	1
9:000170	pin2006	1	CCACATGGTCTAGCACGTG	AACTTTATTCGAGCTTCT	44	58	53	>200	>200	4	4
9:001036	pin1350	2	CATGATACCTCTCGTGGTGA	CCGTTATTTGCTACATGCT	46	84	108	-	-	1	1
9:001081	pin1730	2	AGGCTGAATGTGGCATGCT	CCGTTATTTGCTACATGCT	48	119	119	93	115	1	1
9:001090	pin0931	2	AAAGCATAGAAATACCA	TTCAATATGTTTACCCAGTA	40	90	90	-	-	1	1
9:001213	pin0925	2	TATGTACACAGATGAATAG	TAAATGTAATATCCAGTAA	45	88	88	-	-	1	1
9:001252	pin2010	2	CCAGATGGAAAGGGAAGTCT	CTGGAAATAGAGATCAACAG	47	125	125	150	>200	1	1
9:001268	pin0915	2	TCGAGTTTGTCTCTAATA	GGAAATATCGCTTCAGTTG	43	103	103	-	-	1	1
9:001438	pin2093	2	AGTCTCTTGGCTCTCAT	TATGTCAGTGCCTTTATG	52	137	137	>200	-	1	1
9:001442	pin2435	2	TTTTGTACCTACGTAGAGTACT	ATCCGTCACACATAGTGA	45	105	108	-	-	1	2
9:001453	pin1671	2	TTATTAGGAGCATATTATGTG	ATGTACATTTTGGTATGTAGG	45	67	65	>200	>200	1	2
9:001535	pin1245	2	TTGGTTCCCGCTCTCAAT	ATGATATTATTAGGACGAA	45	75	75	170	190	1	1
9:000875	pin1216	2	ATCTACGTGTTTGTGAGTG	ACTGATTTGTGCTCCATCTG	44	68	67	-	-	1	1
9:001449	pin0449	3	CCACATTTCACTCTCAT	GCGCCACGTAGTACATGTC	43	68	65	-	-	3	6
9:001758	pin1758	3	TCTGGCTCTTTGGTGTGGA	ATGTATACAAATCCAAAG	51	115	115	-	-	1	1
9:001218	pin2434	3	AAAGAAACACATCGCTAA	ATGTATACAAATCCAAAG	42	90	90	-	-	1	1
9:001219	pin0660	3	GTAGTCTCTGCCCTTTAGC	AAGGATTTGATTTTCTACAT	43	77	77	-	-	1	1
9:001277	pin1729	3	GGTCTGTTATTTTGACAT	AAACAGAGAATGTTTCAGA	43	75	75	155	>200	1	1
9:001306	pin1822	3	GATCCTTGTTGTAGTTTCAGTC	CTGCAAAATACAGGAAATCAT	46	83	83	160	140	1	1
9:001418	pin2209	3	ACCCCAAGTCCCAATCCAGT	AGACTCCCCAGCCCTTACT	55	105	105	113	>200	1	1
9:001458	pin2455	3	ATCTAGCTGGCTGTAGTATT	TTAAGAGATGAATTTATTTGGT	42	130	130	190	>200	1	1
9:000271	pin1352	4	GTCTTGTGCTATCTGTGTA	AAGCATTTATTTGAGGTTTA	43	90	95	>200	>200	1	3

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Fig. 7

91000148	pm2256	4	GGCCCAATGTTCTCTAGTAT	GTTCAGTTTATTCAGACA	42	62	62	>200	69	1	2
91001052	pm1151	4	GTGCCATGCACTGTGTAT	GTTCATATTCCATCTCAA	43	80	80	-	-	1	1
91001215	pm0988	4	AGAAATTAATAGCATAGT	TAGAGTCAAGTTCGCTGTG	43	100	100	130	-	1	1
91001298	pm2367	4	ATCAAGTTTATTCCTTCA	CATCCCATCATACATAGTC	43	116	116	>200	180	1	1
91000993	pm09041	5	TGCTGAAGAGACAGCAAA	TCTAAGGAGACAGCATC	49	101	102	113	200	1	1
91000598	pm1809	5	ATCGTAAAGCTTATCCACAG	CTAAGAGGCTTGACCTTCAT	45	87	87	>200	>200	1	1
91001085	pm0719	5	TCACCCAGATATTTACAGT	GAGACATAGCAGGTAGAT	44	120	120	-	-	1	1
91001101	pm2364	5	TTACCTTACCGTGTCTTAC	AGACAAATGCCAAMGCG	47	89	89	190	>200	1	1
91001160	pm1160	5	ATTGTGAGTGTCTTACTA	AGAATGAGTCTTTTATTC	43	101	99	>200	>200	1	1
91000053	pm2720	6	ATGTCATAGTCTCCCTTCA	TGCATCTCTATGTCTCT	44	78	78	72	>200	2	3
91001326	pm1154	6	CAITGAGACAGCAACAG	CCGCGCCCTCTCTGAGTA	53	102	104	145	200	1	1
91001424	pm1216	6	TAGCCAAACAGCAAGAG	AAGGAGCTGTGTCAGGTTG	48	65	65	110	>200	1	1
91001457	pm1785	6	TATATGCAATATCCAAAGTCTG	TCTATATTCGTGCTCTATCT	46	90	90	>200	>200	1	1
91001523	pm0285	6	TGTGACGTTGTCTCTCAGT	TTTAAATGTCCTGGTAT	42	86	70	>200	100	1	1
91001525	pm0328	6	GCACCTAAGCCTCCCAAGT	TTTTATATCAGTCCAGAGC	49	138	138	>200	>200	1	1
91001562	pm2619	6	TCTGCATTGACAGAGCAC	TTTGAGATTTATGAGTCATTC	43	62	62	>200	45	1	1
91000624	pm0991	7	GACCTGAAGTGGGGTCTCT	AACTAGCTTTATGGGATTT	45	119	119	>200	-	1	2
91001145	pm0219	7	AGCCAAAGTCGGGCTCATCT	CCACGGACAGTGAATCAT	56	159	155	115	>200	4	4
91001469	pm1102	7	AATCATTTGGCGAGACTGA	AAGACAACTTTATCCAGCA	45	88	88	130	-	1	1
91001579	pm0956	7	TCAGGCAGTCTGCTCAGTA	TTTGCAGGTTATCTGTTA	44	77	76	170	-	1	1
91001707	pm2527	8	AACAGTATTCGTTGTCAGACTAG	TCCATATAGCCGCTCTCAG	47	81	81	105	70	1	1
91001176	pm2527	9	TGCGCTCTATGTTGCTCTAC	AAAAACACAGCACTAAG	48	99	99	118	180	1	1
91001248	pm2708	9	TGTATTGGATTGGATTCTC	CAMAGCAACAGCAGATA	44	95	95	-	85	1	1
91000995	pm0995	97	TTAAGATCACCCCTCATTTG	CTGTGAGTTTGGTTCTTG	43	55	55	-	-	1	1
91001055	pm0959	97	AAGTATTGTGCAAGAGTGA	CACATGCTTATTTGACACT	44	74	74	72	73	1	1
91001157	pm0547	10	TGTGAAATGCTATCTCTCT	GCATCTGTTTCCATATCAGT	45	138	138	>200	>200	2	3
91001268	pm2245	10	ATCCAAACAACTATCTCTCT	ACTATATATCTGCCACT	47	100	100	200	>200	1	1
91000228	pm2664	11	GAAATGCTGGAGATTTCAC	GGAGATCACTCTTCAGCA	42	117	121	134	95	2	2
91001159	pm0880	11	AAAGTGACCTTATGGACAGTGG	TCGAGCCAAAATACCTCTGACT	46	100	100	84	95	1	1
91001315	pm0445	11	AGGGTGAAGGTTATTTTACG	CACATCACTGTGAGAGCTA	50	153	153	>200	160	1	2
91001352	pm2913	11	AMCCCTCTAGTAAAGCATTTG	TTATTAACCAATCCAGTA	47	83	85	-	-	2	2
91001469	pm0559	11	CTGTAAAGTTTTGGAAATATGT	TTTCATTTTCTACCAATTATT	37	47	47	125	53	1	1
91001570	pm2810	11	AGTGTATGGAACACTTTGAG	GTTCATTGTCAGGTGTAGC	42	75	75	145	>200	3	3
91001663	pm2666	12	TCCTCCCTATTCACACCACT	AATGATTCGTAGATAGCA	48	130	130	103	>200	1	2
91001193	pm1193	12	CACAGCAAAAGAAATCATA	ACCTATTTTATTTCTCAC	49	88	88	>200	120	1	2
91001235	pm2790	12	CATCATGTTACAGTCAGAG	CAGTTGTCAAAATGTTTG	46	100	100	-	-	1	1
91031274	pm1355	12	AGATGTCAGTATCTCTCTATG	GAGACACAGCATTAAGCAACC	44	83	82	93	87	1	1
91001308	pm0368	12	CCAAAGTGTAGGTTTACAG	TTCAATAGACCTTGGGTTAC	47	87	87	>200	>200	1	1
91000159	pm2645	13	CTAAGATTATCGGATTCG	AGTATGTTATGGCAGGGA	47	95	95	>200	>200	1	1
					46	104	104	>200	>200	1	2

Fig. 8

9-001044	pm1659	13	TTGTAGCGCTATCAGAGTCA	AGAGACGTTATGCCATCTA	44	103	200	109	>200	100	1
9-001290	pm1731	13	GCTTCTCTGCTGCTGCTG	CGAGTTATCATGGCTATTCTCC	50	122	122	122	>200	190	1
9-001362	pm0118	13	ACTGAATGGAACATAGTCT	TACATTACAGACATGTGA	40	61	61	61	95	103	1
9-001366	pm0364	13	TGCTTAGCTTTCCCTCCCTA	GACCATTCGTGTTCTCTA	45	67	67	67	-	-	1
9-001389	pm0201	13	CATGAACCTGCTCAGACAA	GCCTACTTTAATGGTGACC	51	100	100	100	100	>200	1
9-001492	pm0541	13	AAATGAATGTAATAATAGACT	ATTAGTTTACAGGAGAT	41	72	72	72	74	1	1
9-001367	pm0441	14	GTTTAAAGTTTGAATTTGGG	CATCCACCTCTTACATTTCT	41	77	77	77	>200	180	3
9-001564	pm0207	14	CGTCTAACTCTGAATC	AATGCTCATTTATCTCAG	42	55	55	55	>200	>200	1
9-001376	pm0219	14	ATCAAAATACCTTTAGTTG	ACGATACATTTATGGAGAT	39	69	69	69	-	-	1
9-001339	pm0220	15	TCCCATCCGAGTGGAAAT	TGAGACAAAGAACCCAGT	47	70	70	70	80	150	1
9-000980	pm0985	16	TTGGAATGGAACCTTGCTA	ACTATGCTGCCGTAATGG	48	79	79	79	66	70	2
9-001242	pm1127	16	CCCTTGTTTACAGTCTCA	ACTATGCTGCCGTAATGG	44	105	105	105	103	102	2
9-001516	pm2543	16	ACAGTGTAAATCAAGGTG	TATTAATCTCCCATTCAT	45	70	70	70	>200	-	1
9-000806	pm0913	17	TTTGTGGGACTATGTAAT	TCTGACACTCAAGTGGCAT	45	70	70	70	>200	-	1
9-001015	pm1157	17	CTCTCCAGTCTCTACAG	TCACCTTTATGGGAACCCAG	41	53	53	53	>200	>200	1
9-001156	pm0269	17	ATATTCACCTTCCCATCAT	TAGAACGAATCTGCTGGT	47	77	77	77	140	>200	2
9-001173	pm0202	17	CAGAAATTAAGTCCAGCAT	TCAAATAGCTCTCTCAGC	50	80	80	80	>200	>200	1
9-001301	pm2117	17	AAATCTTGTTTATTTCC	TGATCTGCTCTTTAAGT	45	103	100	100	>200	>200	2
9-001316	pm1878	17	TAAATTTGTGGAATCTCTGGA	GTGATTTAGTGTACATTCG	41	118	118	118	145	200	1
9-001356	pm0511	17	TGTGACAGCAGCTTCAT	ACACATTTGGTTGCTTTAAC	47	100	100	100	95	97	1
9-001495	pm0538	17	CATCTCAGACACAGGAAC	TGCTAGCATTTTATCCACC	45	128	128	128	-	-	1
9-001522	pm0642	17	TGACTGCAATAGGAGTTGT	ACCTAGAGTCCAGAGAAC	40	90	90	90	69	>200	1
9-001078	pm1815	19	GTCTCAGCAGATTTCAGGT	GAACATCCAGTTTATTTCT	46	90	90	90	180	>200	1
9-001417	pm0289	19	TGTTCTCCAGCTTTGAG	ACTTTCTCTTGAGCACCA	45	88	88	88	160	-	1
9-001069	pm1688	19	GGATCAGACCAACAGTGCTG	GTACATTCCTTGCTACAG	48	65	65	65	>200	>200	1
9-001068	pm1879	20	GACCCACCTCGACCTCA	GGAGAGATTGGGAAACCGT	46	50	50	50	-	-	1
9-001146	pm1146	20	GCCATGCTGTAAAGTATGT	TTAAGAAGCAATAGCTAGGATA	54	93	93	93	>200	>200	2
9-001112	pm0112	20	GCCCTTAGGATTCACCTGTC	ACCACCCAGGCTTTTCAGG	48	140	140	140	-	-	1
9-001039	pm0332	20	TGCTGGATGACTTCTACAG	TCCCTATCATGGCTGCTGTT	52	66	66	66	180	>200	1
9-001132	pm0647	20	CTGTGGGTAGCTCTGACCTC	CAATGGCTTAAGAGGACAT	49	59	59	59	59	115	59
9-001158	pm1774	20	TCTGAATGATGTGGAAACA	ATCTAGTCCCAACCCAGTA	49	135	135	135	153	160	1
9-001210	pm1774	20	GGAGCCACATGGATTGATTTG	AACTAGTCCCTGGCACCTC	48	109	109	109	-	-	1
9-001377	pm1235	20	TCCATGTTTATGTGTTA	GGAGCAGATGAACCTTCAC	52	124	124	124	>200	>200	1
9-001395	pm1701	20	AGCCATCTGGTTATGTCTTA	CCCATCTCCACAGGGAGT	44	90	90	90	>200	>200	1
9-001427	pm2101	21	GTGAGTCAATGTACACAG	TTTATGTGCAACAGAGT	54	142	142	142	>200	74	1
9-000378	pm0618	21	CCTTGGTATTAAGATAGAG	ACATTTGGTCTCAATAAGA	45	130	130	130	180	>200	1
9-001444	pm0912	22	GGTGTAGTGTACCAATTTAG	AGTTGACCCCATCTCTGTC	39	58	58	58	145	>200	1
9-001473	pm0911	22	GGTCTTGTCTCCCATCTGT	AGAGCCCAACCAATAGTCC	46	124	124	124	>200	>200	1
9-001473	pm2231	22	TGAGCTGCACTTACCTGTGAGAG	AAGCAGGTGAGTTGGGTTTCT	65	88	88	88	100	125	1
9-001479	pm2328	22	TACAGCCCTCCAGGTAAAC	TTTATCTGCTCACACTACA	50	94	94	94	67	135	2
		22			46	65	65	65	190	>200	1

Fig. 9

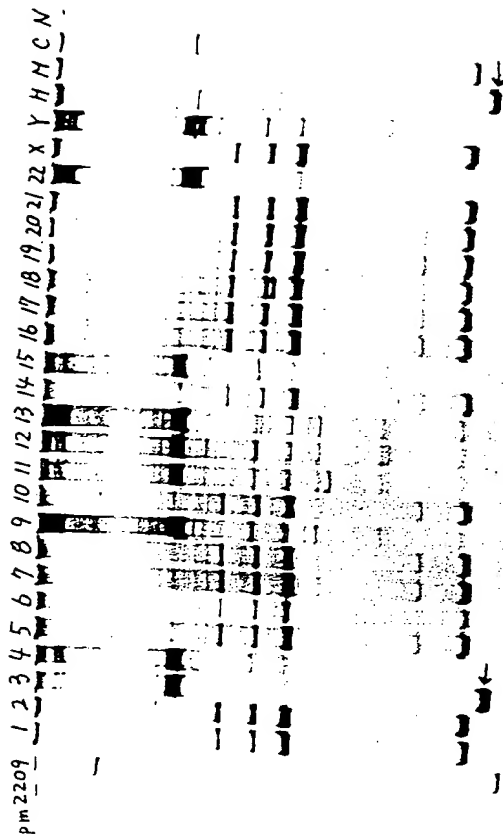
91000999	pm1759	X	CTGCATAGTACCTGGATT	TCACCCACCACTATTAGCA	47	103	-	-	103	-	-	1	1
91001149	pm2180	X	GGAGGGAGATATAGATTGT	AAAAATCCAGAGACTGA	46	70	70	135	150	-	-	1	1
91001161	pm2180	X	TTCATAGTGTGACCACTTT	GTAAAGTTTGAGATACAT	40	85	85	>200	77	1	1	1	1
91001406	pm1291	X	TAATGCCAGTAGTGTTCGTTAA	GTAAGGTTTATCTTGCATCAGA	47	82	82	>200	80	2	3	1	1
91001160	pm2289	1,10	ATCTCGTGAATACATCTG	GGGAGAGACATCATGAC	46	70	70	69	130	1	1	1	1
91001436	pm0113	1,2,12,13,Y	GATCCGATGGAGTGTAAAT	TTTATGTACACAGCACT	44	69	69	170	-	-	-	1	1
91001404	pm2272	1,2,3,5,8,12,14,17,X	TTGGAAATGACATCTCTAT	TACAGTATCCACCACTCA	43	130	130	150	132	2	2	1	1
91000303	pm0314	1,2,6,X	TATCAAGTGAATATGTCAC	AGTTCAGCAGCGGTGAATG	45	93	93	110	-	-	-	1	3
91000140	pm1461	1,3,4,5,8,16	TCCAAATGAGAGGTGTGTTA	AGTTCAGCAGCGGTGAATG	43	96	96	100	100	1	1	1	3
91000336	pm1561	2,20,21,22	GTCTGTCAAGCCCAAGATCCA	TTTATGTGTGTGTCAGT	48	110	110	170	150	1	1	1	1
91001077	pm2795	2,4,5,10,12,15,17,20,22,Y	GACCTGTGACATCTGGACT	TTATATGTGTGTGTCAGT	43	61	61	-	-	-	-	2	6
91001192	pm0913	2,5,14,C	GCCTGTGATTTACACACTC	ATGCCCTTGTCTCCAGTTA	46	82	82	>200	82	1	1	1	1
91000213	pm1853	2,8,12	TCTGAGACATCTCCAGACAG	CAGTCAMACCAACAGGAT	49	95	95	93	160	1	1	1	1
91000919	pm1778	2,9,13,17,X	TGCATAAGGGAAGACCA	CCGTGTAGTGTGATGAATG	49	78	80	>200	>200	1	2	1	2
91000919	pm0885	20,X	GTGATTTGTATGCAATTTCC	GCATACAAATCCCAACT	50	133	133	>200	150	2	2	1	1
91000071	pm0457	3,10,15	CATGTACTCAGAGCACTTC	ACATTTATTTTTCACG	37	45	45	-	-	-	-	1	2
91001126	pm2651	3,4,M	CAGGACTGGACGAGGAAG	GATTTACCCATAGGAAGC	50	101	101	101	88	3	3	1	1
91001391	pm2632	3,6	TTAGMAAATGTGTTAGACAG	ATAGTATTGGTTGACACAGTA	43	80	80	>200	120	1	1	1	1
91000077	pm1133	3,8	TGGATTGCTTACCTTGTT	ACACCTCAGGAGATGTTAC	47	93	93	95	>200	1	1	1	1
91002250	pm2250	3,9,10,15	GCATCAAGCCAAATCAGA	CTTCTTACACCAACAGCAG	50	96	96	>200	125	2	10	1	1
91000605	pm0626	4,6	GGATTCTATTTCGTGTCAT	GTTTATGTAGCGCATTTAC	44	105	100	>200	>200	2	4	1	1
91001212	pm1234	6,20	GCATTAACAGGAACAATA	TTTATAGACATACAGAGGAT	44	110	110	105	107	1	1	1	1
91001441	pm0606	7,18	AGATGCTAACAATFAGGGATA	CCCTACCCACAGCACTCTT	43	81	81	102	-	-	-	1	1
91001357	pm1253	9,11	CCAGACTACAGCGGTATGGC	CCCTACCCACAGCACTCTT	55	75,130	75	>200	>200	1	1	1	1
91001261	pm0115	9,M	ACCAATGTCACCTCTCTAAMATA	CCCATATAAGTGAAGAGGTAGTTC	48	125,155	127	135	>200	1	1	1	1
91001456	pm0428	10,15,22	AAGAAATGTTTACTGGATT	TTATCTGACTGGAGGAAT	42	107	107	-	-	-	-	1	1
91000590	pm2420	10,15,22	ACTACCCCTGAGATATTGTT	TTCAATTATTGATGTTGA	46	100	100	170	-	-	-	1	1
91000314	pm2303	11,M	ATCAGCTCCGCTGTGACCG	GAGGAGGCTCTACTGTCTT	50	72	74	72	>200	3	20	1	1
91000103	pm2613	12,19	GCACCAAGAGCAGTCTCCAG	TTGGGAATGAGAAATACAT	46	83	83	81	-	-	-	1	7
91001487	pm2773	12,M	GATCTGATCTCGCTTTATT	TACATACAAAGATGCAACAGT	44	80	80	79	68	1	1	1	1
91000976	pm2725	13,16	ATCTGTGTGCTGCTTTC	GTCTCTCTCTGATGGCTGA	46	62	60	135	180	1	1	1	1
9100135	pm2780	14,16	AACCTGTTTACCGCATCTT	AGGTATTGTCCACAGAA	46	87	87	>200	>200	1	1	1	1
91001393	pm1693	17,20,C	TGTTGGTCCACCATTAGAC	AGACACACATCAAGATGCC	46	90	90	>200	90	1	1	1	1
91000356	pm1748	17,22,Y	GAAATGTCATCCAAAGCTGAG	CTAGTTATATCTGGCTGTG	44	81	81	>200	200	1	1	1	1
91001369	pm2217	17,C	TTTATCCCAAGCAGCACAC	TCCTCTGCTGCTCTCTTC	49	120	120	>200	170	4	11	1	1
91001440	pm1213	17,C	ACTTAAGTACCTTTGTAGC	TGCCCTGCTGCTCTCTTC	43	95	95	>200	95	1	1	1	1
91001217	pm1118	18,C	CCCCAGTTAAGATATTGTT	TGCCTGCTGCTGCTCTCTTC	44	92	92	-	-	-	-	92	1
91001009	pm2824	19,20	TGCAGAGTGAATTTCCAGAC	AGTGACGATGGAAGGATGTA	46	75	72	160	65	1	1	1	1
91001172	pm0887	19,22	ATCCCTGCTGTCTATTCACAG	GCCTGTTTATGACTCTAC	46	110	110	130	170	2	2	1	1
		19,22	GCCTGCACTGCTGTGTGACTT	AACCTCTGGACAAATCAT	48	91	89	160	86	1	1	1	1

Fig. 10

91001057	pm12049	C	AGGACACAAACACGAGCTAT	TTTCTGATTAGATGAC	45	75	75	101	75	1
91000173	pm11753	M	ATCTTTTGTAGGCACTCTG	GTTAAGTCTGATGCCATT	42	64, 100	64	64	>200	1
91001096	pm12326	M	GTAGAGCTGCTTACTACAC	ACAGACAAAGGAATACATA	42	100, 96	110	110	112	1
91001166	pm10506	M	GTCCACAGTCCAGCCTAAC	GCCACATATTAGATCCATC	46	74	74	74	>200	1
91001151	pm12354	M	TGCTTTTGGAGCTCTGCT	TTTAACAGTCAATTAACATGTT	44	110	110	110	106	1
91000253	pm12492	M1,C	GCTAGAMAGAGGCGCTCA	CTTAAGTCCGATGCCAGGTC	46	75	75	75	75	1
91000285	pm12786	M1,C	CACAAACAGCAAACTTACG	ATGGTTATTTATCAGATTG	41	83	83	82	83	2
91000302	pm11704	M1,C	TCCACCCAGAGACGACAT	AATTCATAGGAATAGGTTG	40	75, 130	75	75	75	3
91000543	pm12318	M1,C	TCGAGAGGACAAATACACC	GAACAGGGTATGCTCCATCG	48	58	58	58	58	1
91000675	pm11699	M1,C	CATGAGGCTACGGAACAGG	AGGATCCGCTGGGCTTTGAG	51	81	84	84	84	1
91000732	pm11442	M1,C	AAGCATCTGAGAGGAACA	GGAGAGCTCGCTGGTCTTGA	49	110, >200	110	110	110	4
91000795	pm11452	M1,C	GCAGCAGATACCTTACACC	TGGTTCACTGACTCTTTC	51	102	105	102	102	3
91001016	pm12668	M1,C	GAGGCTCTGTGAGGAAGT	CCAGACCCCATCTTTATACC	47	79	79	79	79	3
91001053	pm12783	M1,C	AGATGATGCTGGGTGAGAGA	TCAAACTTTAATATGCT	40	93	93	91	92	1
91001127	pm11144	M1,C	ACTGGTATCAGGATGATG	CCATTCTGTGATTCAGATT	52	135	140	135	135	1
91001167	pm12230	M1,C	GAGAGGCTTGCATCGTTA	CCACACAGTGAACACGCTCT	47	55	55	55	55	1
91001216	pm11626	M1,C	TAGTCAGAGATCAGTAAGT	CTTCCCTTGGTCTTCTGTT	49	100	100	100	100	1
91001253	pm12109	M1,C	AACTGGTCCATCAAGACTG	ACATGTTATTTGATAGTCT	42	110	110	110	110	1
91001281	pm11240	M1,C	ACTTAAACCCACCCACAT	AGTGAATAACTCTCCACTCC	48	120	120	120	120	2
91001375	pm10952	M1,C	AAGAGGATTTCCCTGCTCA	ATCATGGCAGATGCAAGGA	47	97	97	97	97	1
91001356	pm12216	M1,C	ATCTCATGACCTATATCT	CGTCTCTTTATTGACAT	51	89	89	89	150	1
91001411	pm10958	M1,C	ATGGGTTATCAGGGGTTTC	GAGACAAAGGCAGCTCTTA	45	108	108	108	108	1
91001460	pm12626	M1,C	ACATGAATGGGATGAGGT	GGACATTTCTAGCCACAGC	51	75, 55	75	75	75	1
91001482	pm11210	M1,C	TTGTGACATCTCTTTAGAA	CAGTGGCTCTGTACTAGAGA	46	85	85	85	85	2
91001450	pm10109	M1,C	GCCCACAGACATCATCT	TCTTAGTAGGTCCTGCTG	51	98	98	98	98	1
91001688	pm12042	No product	CACCAAGTATAGCTGAAGT	GAAATATCCTGTGATCTA	45	87	87	87	87	1
91000950	pm10304	No product	CTTGGGATTTCTTCTCAT	CCCTCGGAGTCTTCTATG	43	60	60	62	62	1
91000961	pm10800	No product	AGCCAGCCTCTTCTTATG	CTGGATTTGATTTCTATG	44	87	87	87	112	1
91001254	pm1673	No product	TGTTGATGAATAATCTGA	TTAATGAATGAACAACAT	43	98	98	163	>200	1
91001355	pm10361	No product	CAGTATGCTCTTGAAGTG	TTTATGGAATGTGGTGT	41	63	63	150	3	3
91001373	pm10849	No product	TACAGCCCTCTCTAAAGTG	TTTGAGCATCAGGAATCT	46	82	82	82	>200	1
91001556	pm1284	No product	TACATCTCTCAGACTATCG	TTTTCAAAAATCTTATCT	40	86	86	86	>200	1
91001574	pm10849	No product	ATCAGAGCTCAGTCTCTGAG	ATTTTGCTCTTGATGGTTC	44	57	57	67	67	2
91001622	pm11606	No product	GATCTGAGCCTTAACTGGA	TTTTCAGTTCAGCTTATTC	45	54	54	54	54	1
91001640	pm10852	No product	GATCTGCTCTCTTTTACA	TTTATACAAAGACCATAC	36	45	45	45	45	1

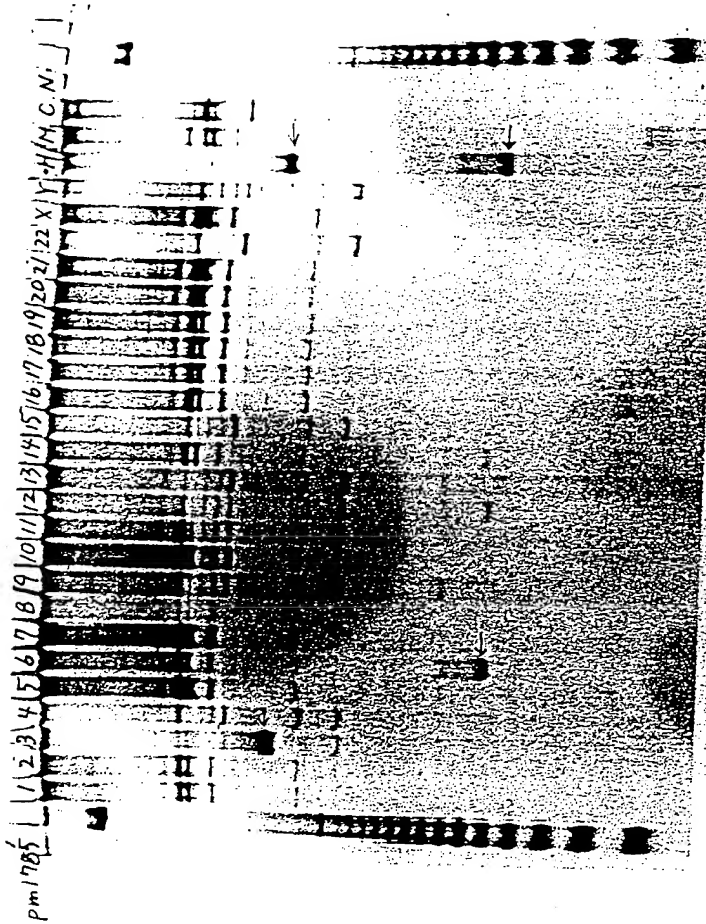
08/530,112

Fig. 11



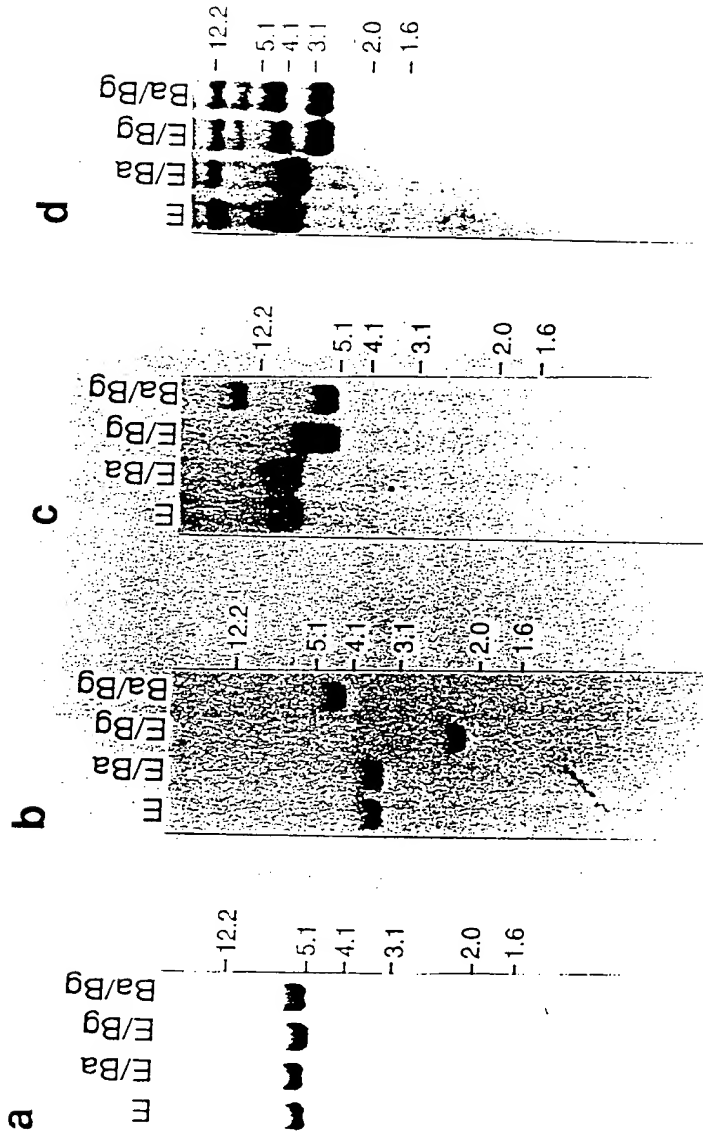
08/530,112

Fig. 12



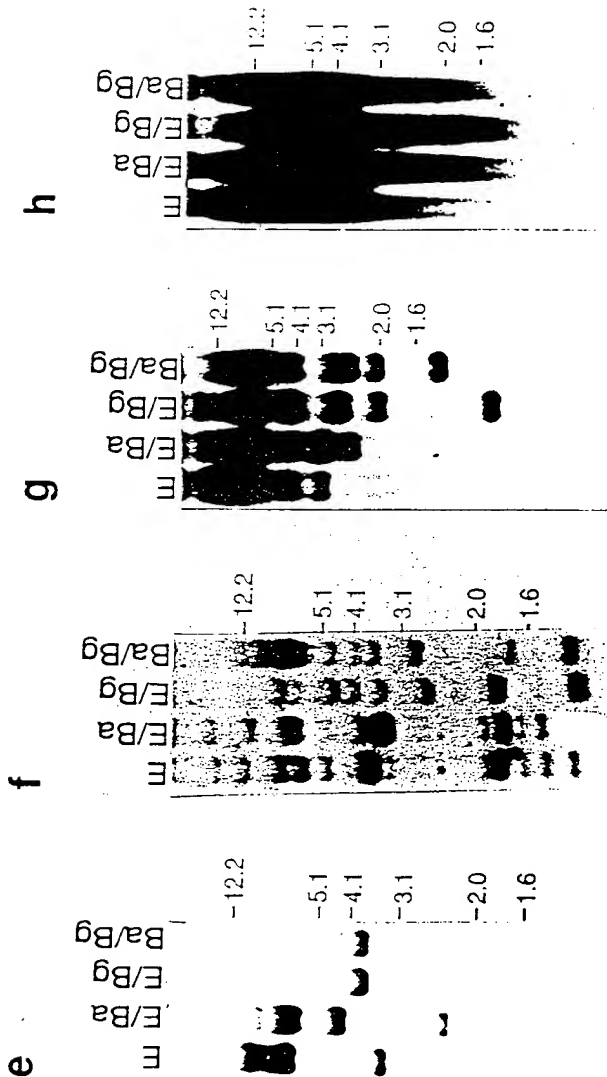
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Fig. 13



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Fig. 14



02/530,112

Fig. 15

Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome	Parent cell No.	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (8)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	75
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A *	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868 *	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11418 *	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10493	17	LTMK	30 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	81 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	81 (10)	0
GM06317	Y	CHW1103	91 (0)	9

550723 2442589

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a

Chromosome



Fig. 16

b

Chromosome

H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

12 →

- 12.2
- 5.1
- 4.1
- 3.1
- 2.0
- 1.6
- 1.0

Fig. 17

550120 2500000

009 100 0

08/530,112

Fig. 18

C

Chromosome



08/530,112

Fig. 19



H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

7 →
7 →
2 →
17 →

- 12.2
- 5.1
- 4.1
- 3.1
- 2.0
- 1.6
- 1.0

e

Chromosome

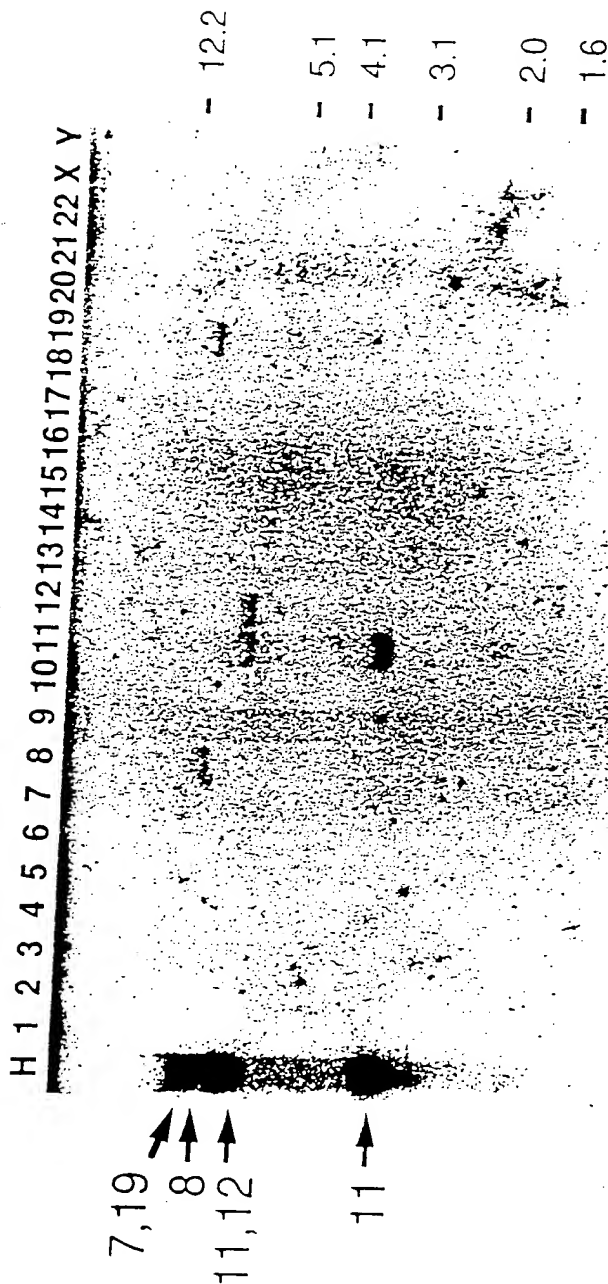


Fig. 20

550729 23 000000

f

Chromosome

H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

1
1
1
1,4
17

- 12.2
- 5.1
- 4.1
- 3.1
- 2.0
- 1.6
- 1.0

Fig. 21

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5507.43 24.00000

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CHROMOSOME

g

Chromosome

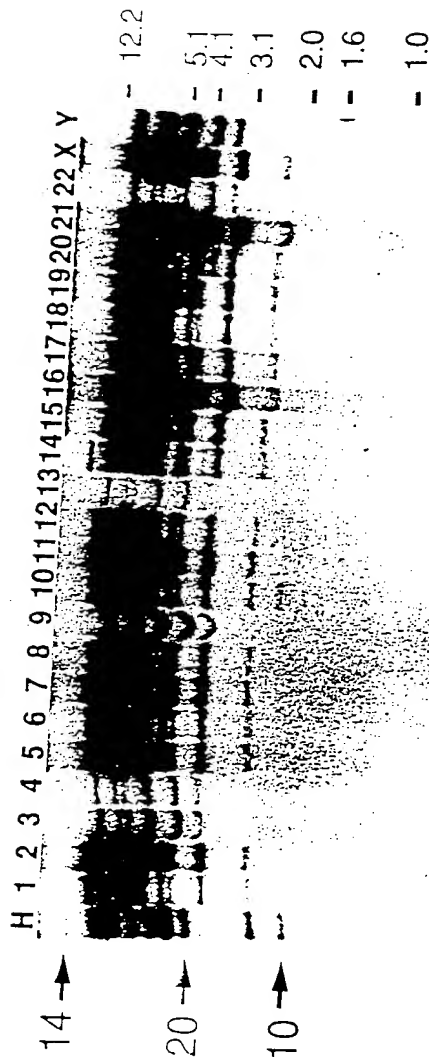


Fig. 22

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Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Numbers of bands detected with human whole chromosomes		Chromosomes assigned				Background	
Clone	Sequence length	≡	≡/B ₁	≡/B ₂	≡ ₁ /B ₂	Mouse	Chinese hamster
Single band group:							
c12c11	GS000075	432	1	1	1	9	0
c12c06	GS000082	540	1	1	1	6,15	0
c12g01	GS000280	212	1	1	1	2	1
c13c05	GS000117	359	1	1	1	11+	0
c13c07	GS000120	355	1	1	1	2	0
c13f10	GS000206	267	1	1	1	14	0
c13h01	GS000279	183	1	1	1	12+	0
c13h02	GS000222	167	1	1	1	6	0
d0g02	GS000095	397	1	1	1	3	0
d0h07	GS000164	313	1	1	1	11	1
d1b10	GS000348	153	1	1	1	20	0
hm01a12	GS000223	246	1	1	1	Y?	0
hm01c09	GS000423	157	0	1	1	1	0
hm01c12	junk	394	1	1	1	17	0
hm01f05	GS000068	454	1	1	1	19,22	0
hm01f10	GS000299	173	0	1	1	10	0
hm01g09	GS000053	477	1	1	1	6	0
hm01h07	GS000115	363	1	1	1	12	0
hm02a02	GS000130	344	1	1	1	4	0
hm02a04	GS000329	164	1	1	0	10	0
hm02c01	GS000203	271	1	1	1	16	0
hm02c01	GS000015	590	1	1	1	20	0
hm02c02	GS000342	156	0	1	1	14	0
hm02c03	GS000401	223	1	1	0	n.d.	0
hm02g02	GS000191	278	1	1	1	17	0
hm05a05	GS000251	219	1	1	1	6	2
hm05a10	junk	392	1	1	1	1	1
hm05c10	GS000009	606	1	1	1	1	0
kmd01	junk	169	1	1	0	n.d.	0
s105	GS000001	703	1	1	1	5	0
s110	GS000057	471	1	1	1	3	0
s11d11	GS000307	#175	0	0	0	7	0
s11h01	GS000269	204	1	1	1	3	0
s147	GS000060	461	1	1	0	2	0
s14c06	junk	639	1	1	1	1	0
s14g02	GS000152	322	1	1	1	4	0
s14h12	GS000271	193	1	1	1	4	1
s150	GS000143	330	1	1	1	17	0
s156	GS000002	306	1	1	1	2	1
s15b11	GS000250	221	1	1	1	14	0
s179	GS000275	196	1	1	1	n.d.	0
s246	GS000234	241	1	1	1	9	0
s247	GS000247	153	1	1	1	1	0
s270	junk	135	1	1	1	19	0

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Fig. 24

Numbers of bands detected with human whole chromosomes				Chromosomes assigned				Background	
Clone	Sequence length	E	E/B ₁	E/B ₃	B ₁ /B ₃			Mouse	Chinese hamster
s306	GS000256	205	1	1	0	1	X	0	0
s309	GS000171	305	1	1	0	1	1	0	0
s342	GS000223	165	1	1	1	1	4	3	2
s331	GS000255	207	1	1	0	1	6,15	1	1
s334	GS000165	312	1	1	1	1	1	0	0
s337	GS000276	195	1	1	1	1	17	0	0
s339	GS000295	130	1	1	1	1	n.d.	0	1
s443	GS000330	251	1	1	1	1	n.d.	0	0
s470	junk	251	1	1	1	1	17	0	0
s474	GS000192	273	1	1	1	1	5	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	GS000334	161	1	1	1	1	14	1	1
s632	junk	587	1	1	1	1	2	0	0
s633	GS000188	311	1	1	1	1	22	2	1
s650	GS000041	644	1	1	1	1	12	1	1
tw1-04	GS000025	537	1	1	1	1	3,7	0	0
tw1-19	GS000213	255	1	1	1	1	17	0	0
tw1-32	junk	250	1	1	1	1	5	0	0
tw1-37	GS000227	235	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	3	1	1
tw1-43	GS000093	173	1	1	1	1	14	0	0
tw1-96	GS000133	339	1	1	1	1	11	0	0
Two band group:									
cl2f12	GS000195	277	1	2	2	2	1,	1	1
cl3d02	GS000042	503	2	2	1	1	2,	0	0
hm01a06	GS000129	344	2	2	2	2	11,13	3	5
hm01a07	GS000207	269	2	2	2	2	7,	0	0
hm01d05	GS000232	243	2	2	2	1	2,	0	0
hm01e01	GS000181	292	2	2	2	2	1,2	0	0
hm02a03	GS000435	302	2	2	2	2	3,	1	1
hm02c04	GS000221	253	2	2	2	2	3,	0	0
hm02c05	GS000146	332	2	2	2	2	17,19,22	0	0
hm05f07	GS000043	503	1	1	2	1	3,	0	0
sl1d06	GS000268	205	2	2	2	2	11,12	0	0
sl1g12	GS000337	255	2	2	2	2	6,	0	0
sl124	GS000083	404	2	2	2	2	9,	1	1
sl144	GS000132	342	1	2	2	2	1,7	0	0
sl14f03	GS000239	243	1	2	2	2	2,	3	2
sl15e02	junk	439	2	2	1	2	6,	0	0
sl16b09	junk	420	1	1	1	2	10,14	0	0
sl17c09	GS000248	223	2	2	2	2	14,	0	0
sl211	junk	284	2	2	2	2	11,	0	0
sl254	GS000124	353	2	2	2	2	1,	3	1
sl255	GS000235	239	2	2	2	2	11,	0	0
sl272	junk	195	2	2	2	2	10,16	1	1

Fig. 25

Numbers of bands detected with human whole chromosomes						Chromosomes assigned	Background		
Clone	Sequence length	E	E/B ₁	E/B ₂	B ₁ /B ₂		Mouse	Chinese hamster	
s311	GS000092	333	1	1	2	2	16.	1	1
s313	junk	132	2	2	1	0	20.	0	0
s317	GS000100	339	0	0	1	2	14,14	1	1
s336	GS000134	337	2	2	2	2	12,14	0	0
s338	GS000139	233	2	2	2	1	22,X	0	0
s339	GS000233	137	2	1	1	2	17.	0	0
s394	GS000063	449	2	1	2	2	13,14	0	0
s396	junk	277	2	2	2	2	17.	0	1
s455	junk	452	1	2	2	1	4.	0	0
s456	GS000236	132	2	2	2	2	8,10	1	2
s465	GS000201	274	1	1	2	2	6,15	0	0
s635	junk	260	1	1	1	2	9,13	0	0
s639	GS000257	205	1	2	2	2	2,X	0	0
s656	GS000025	#590	2	2	0	2	6,11	0	0
tw1-33	junk	352	2	2	2	2	1.	0	0
tw1-39	GS000153	#321	2	2	2	2	17.	0	0
tw1-70	GS000061	441	1	1	2	1	11.	0	0
tw1-80	junk	453	2	2	1	2	9,17	2	2
tw1-87	GS000153	316	2	2	2	2	7.	0	0
Three band group									
d0h06	GS000030	417	3	3	3	1	1.	0	0
hm05b07	junk	336	2	3	3	3	5.	0	0
hm05g02	GS000209	267	2	2	2	1	3,17,19	1	1
s129	GS000107	373	3	3	3	3	n.d.	1	1
s173	GS000357	146	1	2	2	3	2.	0	0
s17a10	GS000294	181	3	3	3	3	2,13,22	1	1
s308	GS000412	638	2	2	2	3	XX	1	1
s401	GS000224	249	2	3	3	3	6,6.	0	0
s654	GS000045	491	3	3	3	3	1,22.	0	0
tw1-32	GS000208	267	3	3	3	3	13.	4	0
Four band group									
c12g07	GS000134	320	4	4	2	3	5, 14.	0	0
c13a08	GS000055	508	3	3	4	4	2,7,7,17	1	2
c13c04	GS000106	#376	4	3	3	3	n.d.	0	2
c13c09	GS000302	195	4	2	4	4	2,17.	7	2
s136	GS000160	315	4	4	4	4	4,X.	2	1
s163	GS000004	#613	4	4	4	2	4,4,8,20	3	1
s479	GS000130	293	4	4	2	2	7,8,11,11,12,19	0	0
Group with 5 or more bands									
c12f08	GS000253	217	5	5	5	2	2,7,9,14.	2	0
hc01	junk	374	12	12	15	13	1,2,6.	22	20
hd10	junk	361	4	4	4	3	n.d.	12	6
he10	junk	173	6	2	3	3	6,3,9,19,21.	3	3
hm01c05	GS000305	176	9	7	5	5	X	9	8
hm01f04	GS000246	215	8	10	5	5	n.d.	12	12
hm01g02	junk	411	9	6	6	4	10,14,20.	14	6

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Fig. 26

Numbers of bands detected with human whole chromosomes						Chromosomes assigned	Background		
Clone	Sequence length	E	E/B ₁	E/B ₂	B ₃ /B ₂		Mouse	Chinese hamster	
hm02f09	GS000273	442	8	7	7	5	3,3,6,11,13,14,15,16	0	0
hm05a02	GS000098	373	5	6	4	6	2,3,17,	3	3
hm05a04	GS000236	#239	6	6	6	7	n.d.	8	5
kmb01	junk	350	3	5	5	5	13,	14	7
s11f06	GS000316	170	6	6	6	4	1,2,2,3,4,6,13,15,	0	3
s14f01	GS000407	262	12	11	10	9	1,6,9,13,	6	3
s173	GS000094	397	5	4	6	8	1,1,1,1,4,17	0	0
s255	GS000323	167	10	12	11	14	13,	9	5
s341	junk	494	9	9	8	6	n.d.	15	8
s406	GS000113	364	6	7	5	4	2,7,8,13,20,20	4	1
tw1-46	junk	593	9	10	10	10	1,1,2,2,5,11,X,	3	5
tw1-63	junk	203	8	10	10	12	3,4,	17	11
Bands no detected:									
cl3g02	GS000340	157	0	0	0	0	-	-	-
hm01e10	junk	232	0	0	0	0	-	-	-
hm02d11	GS000274	196	0	0	0	0	-	-	-
s323	GS000273	194	0	0	0	0	-	-	-
s359	GS000199	279	0	0	0	0	-	-	-
s511	junk	233	0	0	0	0	-	-	-
s645	GS000012	#734	0	0	0	0	-	-	-
s647	GS000105	360	0	0	0	0	-	-	-
s651	junk	540	0	0	0	0	-	-	-